RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____10/684,237_____

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RAW SEQUENCE LISTING   DATE: 03/24/2006
PATENT APPLICATION: US/10/684,237   TIME: 08:38:34

        Input Set : N:\Crf3\RULE60\10684237.raw
        Output Set: N:\CRF4\03242006\J684237.raw

  1 <110> APPLICANT: Huston, J.
  2   Houston, L.L.
  3   Ring, D.
  4   Oppermann, H.
  5 <120> TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
  6 <130> FILE REFERENCE: CIBT-P01-130
  7 <140> CURRENT APPLICATION NUMBER: US/10/684,237
  8 <141> CURRENT FILING DATE: 2003-10-10
  9 <150> PRIOR APPLICATION NUMBER: US/09/558,741
 10 <151> PRIOR FILING DATE: 2000-04-26
 11 <150> PRIOR APPLICATION NUMBER: 07/831,967
 12 <151> PRIOR FILING DATE: 1992-02-06
 13 <160> NUMBER OF SEQ ID NOS: 16
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 909
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Artificial Sequence
 20 <220> FEATURE:
 21 <223> OTHER INFORMATION: 741F8 sFv'
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (3)..(752)
 25 <223> OTHER INFORMATION:
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 27   cc atg gcg gag atc caa ttg gtg cag tct gga cct gag ctg aag aag   47
 28   Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
 29   1   5   10   15
 30   cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc   95
 31   Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 32   20   25   30
 33   aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta   143
 34   Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
 35   35   40   45
 36   aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct   191
 37   Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala
 38   50   55   60
 39   gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc   239
 40   Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
 41   65   70   75
 42   act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca   287
 43   Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr
 44   80   85   90   95

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46        Tyr Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp
47                        100                 105                 110
48        ggc caa ggg act ctg gtc act gtc tct gca tcg agc tcc tcc gga tct        383
49        Gly Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser
50                        115                 120                 125
51        tca tct agc ggt tcc agc tcg agc gat atc gtc atg acc cag tct cct        431
52        Ser Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro
53                        130                 135                 140
54        aaa ttc atg tcc acg tca gtg gga gac agg gtc agc atc tcc tgc aag        479
55        Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys
56            145                 150                 155
57        gcc agt cag gat gtg agt act gct gta gcc tgg tat caa caa aaa cca        527
58        Ala Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
59        160                 165                 170                 175
60        ggg caa tct cct aaa cta ctg att tac tgg aca tcc acc cgg cac act        575
61        Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr
62                        180                 185                 190
63        gga gtc cct gat cgc ttc aca ggc agt gga tct ggg aca gat tat act        623
64        Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr
65                        195                 200                 205
66        ctc acc atc agc agt gtg cag gct gaa gac ctg gca ctt cat tac tgt        671
67        Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys
68                        210                 215                 220
69        cag caa cat tat aga gtg ccg tac acg ttc gga ggg ggg acc aag ctg        719
70        Gln Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu
71            225                 230                 235
72        gag ata aaa cgg gct gat ggg gga ggt gga tgt taacggggga ggtggatgtt      772
73        Glu Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
74        240                 245                 250
75        gggtctcgtt acgttgcgga tctcgaggct atctttacta actcttaccg taaagttctg      832
76        gctcaactgt ctgcacgcaa gcttttgcag gatatcatga gcgcttaaga tccgtcgacc      892
77        tgcaggcatg caagctt                                                     909
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79 <210> SEQ ID NO: 2
80 <211> LENGTH: 250
81 <212> TYPE: PRT
82 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: 741F8 sFv'
85 <400> SEQUENCE: 2

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86        Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro
87        1               5                   10                  15
88        Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
89                        20                  25                  30
90        Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys
91                    35                  40                  45
92        Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu
93                50                  55                  60
94        Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr
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```
95      65                      70                      75                      80
96      Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr
97                      85                      90                      95
98      Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly
99                      100                     105                     110
100     Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser
101                     115                     120                     125
102     Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys
103                 130                     135                     140
104     Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala
105     145                     150                     155                     160
106     Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly
107                     165                     170                     175
108     Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
109                 180                     185                     190
110     Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu
111                 195                     200                     205
112     Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln
113         210                     215                     220
114     Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
115     225                     230                     235                     240
116     Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys
117                 245                     250
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 779
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: 26-10 sFv'
125 <220> FEATURE:
126 <221> NAME/KEY: CDS
127 <222> LOCATION: (3)..(758)
128 <223> OTHER INFORMATION:
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130     cc atg gaa gtt caa ctg caa cag tct ggt cct gaa ttg gtt aaa cct      47
131        Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro
132        1                   5                   10                  15
133     ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc      95
134     Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr
135                     20                      25                      30
136     gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac     143
137     Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp
138                 35                      40                      45
139     tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag     191
140     Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln
141                 50                      55                      60
142     aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act     239
143     Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr
144                 65                      70                      75
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145    gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac    287
146    Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
147    80              85              90              95
148    tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt    335
149    Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly
150            100             105             110
151    cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt    383
152    His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly
153            115             120             125
154    tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct    431
155    Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser
156            130             135             140
157    ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc cgc tct tcc    479
158    Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser
159            145             150             155
160    cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg    527
161    Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu
162    160             165             170             175
163    caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac    575
164    Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn
165            180             185             190
166    cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act    623
167    Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
168            195             200             205
169    gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc    671
170    Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile
171            210             215             220
172    tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc    719
173    Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly
174            225             230             235
175    acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc    768
176    Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
177    240             245             250
178    ccgggggatc c                                                      779
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181 <211> LENGTH: 252
182 <212> TYPE: PRT
183 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: 26-10 sFv'
186 <400> SEQUENCE: 4
187    Met Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
188    1               5               10              15
189    Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp
190            20              25              30
191    Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr
192            35              40              45
193    Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys
194    50              55              60
```

```
195     Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala
196     65                  70                  75                  80
197     Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
198                     85                  90                  95
199     Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His
200                     100                 105                 110
201     Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser
202                     115                 120                 125
203     Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu
204                     130                 135                 140
205     Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln
206     145                 150                 155                 160
207     Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln
208                     165                 170                 175
209     Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg
210                     180                 185                 190
211     Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
212                     195                 200                 205
213     Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr
214                     210                 215                 220
215     Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr
216     225                 230                 235                 240
217     Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys
218                     245                 250

220  <210> SEQ ID NO: 5
221  <211> LENGTH: 739
222  <212> TYPE: DNA
223  <213> ORGANISM: Artificial Sequence
224  <220> FEATURE:
225  <223> OTHER INFORMATION: 520C9 sFv
226  <220> FEATURE:
227  <221> NAME/KEY: CDS
228  <222> LOCATION: (1)..(729)
229  <223> OTHER INFORMATION:
230  <400> 5
231     gag atc caa ttg gtg cag tct gga cct gag ctg aag aag cct gga gag    48
232     Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
233     1               5                   10                  15
234     aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat    96
235     Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
236                     20                  25                  30
237     gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg    144
238     Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
239                     35                  40                  45
240     ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc    192
241     Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe
242     50                  55                  60
243     aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat    240
244     Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His
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`W--> 230` (marker at left of line 230)

VERIFICATION SUMMARY
DATE: 03/24/2006

PATENT APPLICATION: **US/10/684,237**
TIME: 08:38:35

Input Set : **N:\Crf3\RULE60\10684237.raw**
Output Set: **N:\CRF4\03242006\J684237.raw**

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L:129 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:0
L:230 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:0
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